#12

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
ELLMEIER, WILFRIED
LANDAU, NATHANIEL R.
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(ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
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(D) STATE: New Jersey
(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:09/734,221
(B) FILING DATE:2000/12/11
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/666,020
(B) FILING DATE: 19-JUN-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/227,319
(B) FILING DATE: 13-APR-1994

(viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 1049-1-004 N2

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGATCCG GTGGAACAAG ATGGATTAT 29

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCGTCGACA TGTGCACAAC TCTGACTG 28

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC 60

CAAAAA 66

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15

Ser Glu Pro Cys Gln Lys
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCCAGAT 60
TATGCTTCGG AGCCCTGCCA AAAA 84

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Pro Tyr
1 5 10 15

Asp Val Pro Asp Tyr Ala Ser Glu Pro Cys Gln Lys
20 25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCAATTATC CATACGATGT TCCAGATTAT GCTTCGGAGC CCTGCCAAAA A 51

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGGATCCA CCATGGATTA TCAAGTGTCA AGTCCAATCT ATGACATCAA TTATCCATAC 60
GAT 63

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATACGATG TTCCAGATTA TGCT 24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCATACG ATGTTCCAGA TTATGCTTCG 30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAGATGGAT 60
TATCAAGTGT CAAGTCCAAT CTATGACATC AATTATTATA CATCGGAGCC CTGCCAAAAA 120
ATCAATGTGA AGCAAATCGC AGCCCGCCTC CTGCCTCCGC TCTACTCACT GGTGTTCATC 180
TTTGGTTTTG TGGGCAACAT GCTGGTCATC CTCATCCTGA TAAACTGCAA AAGGCTGAAG 240
AGCATGACTG ACATCTACCT GCTCAACCTG GCCATCTCTG ACCTGTTTTT CCTTCTTACT 300
GTCCCCTTCT GGGCTCACTA TGCTGCCGCC CAGTGGGACT TTGGAAATAC AATGTGTCAA 360
CTCTTGACAG GGCTCTATTT TATAGGCTTC TTCTCTGGAA TCTTCTTCAT CATCCTCCTG 420
ACAATCGATA GGTACCTGGC TGTCGTCCAT GCTGTGTTTG CTTTAAAAGC CAGGACGGTC 480
ACCTTTGGGG TGGTGACAAG TGTGATCACT TGGGTGGTGG CTGTGTTTGC GTCTCTCCCA 540
GGAATCATCT TTACCAGATC TCAAAAAGAA GGTCTTCATT ACACCTGCAG CTCTCATTTT 600
CCATACAGTC AGTATCAATT CTGGAAGAAT TTCCAGACAT TAAAGATAGT CATCTTGGGG 660
CTGGTCCTGC CGCTGCTTGT CATGGTCATC TGCTACTCGG GAATCCTAAA AACTCTGCTT 720
CGGTGTCGAA ATGAGAAGAA GAGGCACAGG GCTGTGAGGC TTATCTTCAC CATCATGATT 780
GTTTATTTTC TCTTCTGGGC TCCCTACAAC ATTGTCCTTC TCCTGAACAC CTTCCAGGAA 840
TTCTTTGGCC TGAATAATTG CAGTAGCTCT AACAGGTTGG ACCAAGCTAT GCAGGTGACA 900
GAGACTCTTG GGATGACGCA CTGCTGCATC AACCCCATCA TCTATGCCTT TGTCGGGGAG 960
AAGTTCAGAA ACTACCTCTT AGTCTTCTTC CAAAAGCACA TTGCCAAACG CTTCTGCAAA 1020
TGCTGTTCTA TTTTCCAGCA AGAGGCTCCC GAGCGAGCAA GCTCAGTTTA CACCCGATCC 1080
ACTGGGGAGC AGGAAATATC TGTGGGCTTG TGACACGGAC TCAAGTGGGC TGGTGACCCA 1140
GTCAGAGTTG TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGGA 1200
GAGGTCTTTT TTAAAAGGAA GTTACTGTTA TAGAGGGTCT AAGATTCATC CATTTATTTG 1260
GCATCTGTTT AAAGTAGATT AGATCTTTTA AGCCCATCAA TTATAGAAAG CCAAATCAAA 1320
ATATGTTGAT GAAAAATAGC AACCTTTTTA TCTCCCCTTC ACATGCATCA AGTTATTGAC 1380
AAACTCTCCC TTCACTCCGA AAGTTCCTTA TGTATATTTA AAAGAAAGCC TCAGAGAATT 1440
GCTGATTCTT GAGTTTAGTG ATCTGAACAG AAATACCAAA ATTATTTCAG AAATGTACAA 1500
CTTTTTACCT AGTACAAGGC AACATATAGG TTGTAAATGT GTTTAAAACA GGTCTTTGTC 1560
TTGCTATGGG GAGAAAAGAC ATGAATATGA TTAGTAAAGA AATGACACTT TTCATGTGTG 1620
ATTTCCCCTC CAAGGTATGG TTAATAAGTT TCACTGACTT AGAACCAGGC GAGAGACTTG 1680
TGGCCTGGGA GAGCTGGGGA AGCTTCTTAA ATGAGAAGGA ATTTGAGTTG GATCATCTAT 1740
TGCTGGCAAA GACAGAAGCC TCACTGCAAG CACTGCATGG GCAAGCTTGG CTGTAGAAGG 1800
AGACAGAGCT GGTTGGGAAG ACATGGGGAG GAAGGACAAG GCTAGATCAT GAAGAACCTT 1860
GACGGCATTG CTCCGTCTAA GTCATGAGCT GAGCAGGGAG ATCCTGGTTG GTGTTGCAGA 1920
AGGTTTACTC TGTGGCCAAA GGAGGGTCAG GAAGGATGAG CATTTAGGGC AAGGAGACCA 1980
CCAACAGCCC TCAGGTCAGG GTGAGGATGG CCTCTGCTAA GCTCAAGGCG TGAGGATGGG 2040

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AAGGAGGGAG GTATTCGTAA GGATGGGAAG GAGGGAGGTA TTCGTGCAGC ATATGAGGAT    2100
GCAGAGTCAG CAGAACTGGG GTGGATTTGG TTTGGAAGTG AGGGTCAGAG AGGAGTCAGA    2160
GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCTTGA AAAGACATCA AGCACAGAAG    2220
GAGGAGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT GGGTCTGGTT    2280
TGCAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTTCACTGA ATGCTTCTGA    2340
CTTCATAGAT TTCCTTCCCA TCCCAGCTGA AATACTGAGG GGTCTCCAGG AGGAGACTAG    2400
ATTTATGAAT ACACGAGGTA TGAGGTCTAG GAACATACTT CAGCTCACAC ATGAGATCTA    2460
GGTGAGGATT GATTACCTAG TAGTCATTTC ATGGGTTGTT GGGAGGATTC TATGAGGCAA    2520
CCACAGGCAG CATTTAGCAC ATACTACACA TTCAATAAGC ATCAAACTCT TAGTTACTCA    2580
TTCAGGGATA GCACTGAGCA AAGCATTGAG CAAAGGGGTC CCATATAGGT GAGGGAAGCC    2640
TGAAAAACTA AGATGCTGCC TGCCCAGTGC ACACAAGTGT AGGTATCATT TTCTGCATTT    2700
AACCGTCAAT AGGCAAAGGG GGGAAGGGAC ATATTCATTT GGAAATAAGC TGCCTTGAGC    2760
CTTAAAACCC ACAAAAGTAC AATTTACCAG CCTCCGTATT TCAGACTGAA TGGGGGTGGG    2820
GGGGGCGCCT TAGGTACTTA TTCCAGATGC CTTCTCCAGA CAAACCAGAA GCAACAGAAA    2880
AAATCGTCTC TCCCTCCCTT TGAAATGAAT ATACCCCTTA GTGTTTGGGT ATATTCATTT    2940
CAAAGGGAGA GAGAGAGGTT TTTTTCTGTT CTTTCTCATA TGATTGTGCA CATACTTGAG    3000
ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC CATCATAGTA CAGGTAAGGT GAGGGAATAG    3060
TAAGTGGTGA GAACTACTCA GGGAATGAAG GTGTCAGAAT AATAAGAGGT GCTACTGACT    3120
TTCTCAGCCT CTGAATATGA ACGGTGAGCA TTGTGGCTGT CAGCAGGAAG CAACGAAGGG    3180
AAATGTCTTT CCTTTTGCTC TTAAGTTGTG GAGAGTGCAA CAGTAGCATA GGACCCTACC    3240
CTCTGGGCCA AGTCAAAGAC ATTCTGACAT CTTAGTATTT GCATATTCTT ATGTATGTGA    3300
AAGTTACAAA TTGCTTGAAA GAAAATATGC ATCTAATAAA AAACACCTTC TAAAATAAAA    3360
AAAAAAAAAA AAAAAAAAAA AAA                                            3383
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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1               5                  10                  15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
            20                  25                  30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
        35                  40                  45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
    50                  55                  60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65                  70                  75                  80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
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85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350